

REMARKS

By this amendment, claims 1, 4, 9, 14 and 15 have been amended, and claims 10, 20, 21, 23, 25, 27 and 28 have been cancelled without prejudice or disclaimer. New claims 29-31 have been added. Claims 1-9, 11-19 and 29-31 are pending in this application.

The attached Appendix includes marked-up copies of each rewritten paragraph (37 C.F.R. §1.121(b)(1)(iii)) and claim (37 C.F.R. §1.121(c)(1)(ii)).

New claim 29 is supported, at least, by the Sequence Listing, page 41, line 24 to page 42, line 7, Figure 10, page 18, lines 11-21 and claim 4 of the specification.

New claims 29 and 30 recite "a nucleotide sequence that is at least 80% identical to..." Support for these claims can be found, at least, at page 18, line 3, page 37, lines 3-5 and page 37, line 22 to page 38, line 2 of the specification. Specifically, page 18, line 3 indicates that the present invention contemplates any sequence that is 80% similar to any one of SEQ ID No's: 1, 3, 5 and 7, while page 37, line 22 to page 38, line 2 discloses that no prior art sequence is more than 73% identical to any one of SEQ ID No's: 1, 3, 5 and 7.

Support for new claim 31 can be found, at least, at Figure 1, Figure 2, Figure 10, page 37, lines 10-20, and the Sequence Listing of the specification.

Applicants have amended the specification so that the phrase "gene of interest" now reads "coding sequence of interest." This amendment has been made to pages 3, 7, 10, 15, 18-23, 27, 31-34, 42, 46, and the abstract.

Applicants have also amended the brief description of Figure 2 (page 7) to correct a typographical error.

The last paragraph on Page 14 has also been amended to correct the references to the SEQ ID NO's for *AtRDP3A* and *3B*, and *AtHD2A* and *2B*. The first paragraph of page 18 has been amended to correct a typographical error.

I. Objections Under Sequence Rules of 37 C.F.R. 1.821-1.825

The Examiner requires that references to sequences in the brief descriptions of Figures 3 and 4 on page 7 include the proper SEQ ID NOs. Applicants have accordingly amended the brief descriptions of Figures 3 and 4 to include SEQ ID NOs where appropriate in reference to any sequences.

II. Claim Objections

The Examiner has noted several errors in the claims. Specifically, Examiner notes that the word "deaceylase" is misspelled at claim 1, line 7 and that claims 14 and 15 are missing a period punctuation mark. Applicant has amended claims 1, 14 and 15 to correct each of the errors noted by Examiner.

III. Claim Rejections Under 35 U.S.C. 112, Second Paragraph

The Examiner has rejected claim 1 under 35 U.S.C. 112, second paragraph for not specifying that the histone deacetylase and the DNA binding protein form a fusion protein. Applicants have amended claim 1 to recite "a histone deacetylase fused with a DNA binding protein."

The Examiner has rejected claim 9 for being a Markush-type claim but employing incorrect Markush terminology. Applicants have amended claim 9 in accordance with Examiner's suggestions for correcting the Markush terminology of claim 9. Applicants have further voluntarily amended claim 4 in the same manner to be in proper Markush form.

The Examiner has rejected claims 4 and 9, alleging that the term "derivative" in line 3 causes a lack of clarity. Applicants have amended claims 4 and 9 to delete the term "derivative."

The Examiner has rejected claim 20 as indefinite for being dependent on a non elected claim. Applicants have cancelled claim 20 without prejudice or disclaimer.

IV. Rejections Under 35 U.S.C. 112, First Paragraph

The Examiner has rejected claims 1-9 and 11-20 under 35 U.S.C. 112, first paragraph, alleging that these claims contain subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor had possession of the claimed invention. Applicants respectfully traverse the rejection.

The Examiner states on page 7, last paragraph, that two fragments of AtHDA have been characterized, and that functional domains other than the "deacetylase domain" are not described. In response Applicants note that Figures 10A and 10B disclose the preparation and characterization of 5 deletion fragments of AtHD2A. The activity of these fragments indicates that at least two domains are required for HD activity, the deacetylase, and HD binding, domains. This is discussed on page 41, line 24 to page 42, line 7 of the specification. The deacetylase domain (amino acids 1-73, Figure 10A) comprises catalytic residues, and the acidic region (amino acids 137-162, Figure 10A) comprises residues that interact with basic tails of histones (see page 28, lines 1-6). Deletion of either of these regions results in the loss of HD activity. These domains are found in AtHD2A, AtHD2B, and ZmHD2, as shown in Figure 4. As mentioned on page 28, line 28 to page 28, line 9, and page 37, line 30 to page 38, line 8, the residues required for catalytic activity, and the acidic domain are conserved in these three HD's, and similar to those domains known in the art (reference to the prior art provided in this text on pages 28 and 37, which are incorporated by reference, page 51, line 9). Therefore, Applicants submit that support is provided for functional activity associated with more than one domain. Furthermore, these functional domains are present in more than one HD, as shown in Figure 4.

Similarly, as stated on page 37, lines 23-28, the residues known to be essential for HD activity (references provided in the text on page 37) are conserved in AtRPD3A and AtRPD3B. Applicants submit that one of skill in the art, with knowledge of the sequences

associated with AtRPD3A and 3B, and those of the prior art may readily obtain fragments of AtRPD3A or AtRPD3B using the methods as described in the present application.

At the top of page 8, line 2 of the Office Action, the Examiner states that only the structures of SEQ ID NO's: 1, 3, 5 and 7 are correlated with repressing transcription. Applicants respectfully disagree. As indicated above, fragments of SEQ ID NO's: 5 and 7 have also been shown to exhibit HD activity as noted on page 28, line 28 to page 28, line 9; page 37, line 30 to page 38, line 8; and page 41, line 24- page 42, line 7 (and Figures 4 and 10). Therefore, Applicants submit that support is provided for a variety of HD and fragments that exhibit repression of gene expression activity.

Applicants have amended claims 4 and 9 to delete the terms "analogue," or "derivative" and to recite the term "fragment" or "deletion."

With regards to hybridization conditions, the Examiner states, on page 8, last sentence of the first paragraph, that the specification does not define the stringency of the hybridization conditions. Applicants disagree, as the text referred to by Examiner (page 18, lines 4-9) are further defined on page 8, lines 11-21. Applicants therefore submit that stringent hybridization are disclosed. As requested by the Examiner, claims 4 and 9 have been amended to recite "wash conditions" as defined in the specification at page 18, lines 20-21. Furthermore, Applicants note that the claims that recite hybridization conditions also stipulate that the nucleic acid that hybridizes under the specified conditions must also exhibit "repression of gene expression activity." This phrase is defined on page 15, lines 9-20 of the specification, and clearly excludes nucleic acids that may hybridize with the specified sequences, and that do not repress gene expression.

In Item 10, the Examiner rejects claims 1-9 and 11-20 under 35 U.S.C. 112, first paragraph. The Examiner specifically takes issue with the phrase "regulating gene expression" recited in the preamble of claim 1 and suggests that the rejection may be

overcome by replacing this phrase with the phrase "repressing transcription of a gene of interest." Applicants have amended claim 1 according to Examiner's suggestion.

The Examiner also takes issue with the term "analogs, derivatives and fragments" and alleges that undue experimentation would be required by one skilled in the art to make and use the claimed invention. As explained above, the specification fully discloses a method by which a person skilled in the art could make and use the invention commensurate in scope with the claims. The specification clearly teaches a person of skill in the art that fragments can be determined by preparing a fusion protein comprising a fragment of a histone deacetylase and a DNA binding protein, and then determining whether the fusion protein can effect expression of a nucleotide sequence of interest associated with a controlling sequence that is specific for the DNA binding protein. The controlling sequence may be placed in operative association with a reporter gene for ease of determination. A person of skill in the art is readily able to follow these steps and determine which fragments exhibit gene repression activity.

As mentioned above, for the purpose of expediting prosecution, claims 4 and 9 now recite the terms "fragment" or "deletion".

Applicants submit that a variety of sequences of HD's have been disclosed in the present application. Furthermore, fragments or deletions of these HD's have been identified and several of these fragments shown to exhibit repression of gene expression activity. Clearly, one of skill in the art may use the teachings of the present application and obtain similar HD's or prepare similar fragments to those that are disclosed and circumvent the claims of the present invention. Therefore, Applicants submit that a range of species has been disclosed, and that a more generic claim scope, commensurate with the teachings of the present application, is warranted.

Reconsideration of the rejection against claims 1-9 and 11-20 under 35 U.S.C. 112, first paragraph, is therefore requested.

V. Rejections Under 35 U.S.C. 102

The Examiner has rejected claim 9, under 35 U.S.C. 102(b), as being anticipated by Tomihama et al. alleging that Tomihama et al. disclosed SEQ ID NO:1 prior to the date of invention.

Applicants have amended claim 9 to delete all occurrences and all references to SEQ ID NO:1 and therefore requests withdrawal of Examiner's rejection to claim 9 under 35 U.S.C. 102(b).

The Examiner has rejected claims 9, 11 and 17-20, under 35 U.S.C. 102(e), specifically alleging that the scope of claim 9 encompasses subject matter taught by Baldwin et al. in US Patent No. 6,287,843. Examiner alleges that sequences and proteins taught by Baldwin et al. are analogs of instant SEQ ID Nos. 1, 3, 5 and 7.

Applicants have amended claim 9 to remove the term "analog" and therefore submits that sequences taught by Baldwin et al. are outside the scope of claim 9 as presently amended. As claims 11, and 17-20 each depend from claim 9, they include the limitations of claim 9. Accordingly, Applicants respectfully request that Examiner's rejection to claims 9, 11 and 17-20 under 35 U.S.C. 102(b) be withdrawn.

VI. Claim Rejections Under 35 U.S.C. 103

The Examiner has rejected claims 1-9 and 11-20, under 35 U.S.C. 103(a), as allegedly being unpatentable over Evans et al. in combination with Baldwin et al. Applicants respectfully disagree.

Applicants submit that Evans et al. does not teach or suggest to one of skill in the art a method to repress gene expression of a sequence of interest in a transgenic plant as defined in claim 1. Rather, Evans et al., as described on page 3 lines 12-19 of the specification, is

directed to the regulation of gene expression in animal systems. One of skill in the art would not have been lead to the method as defined in claim 1, and claims depending from claim 1, upon reading of Evans et al. Furthermore, Evans et al. does not teach or suggest the nucleotide sequences defined in claim 9.

Similarly, Baldwin et al. does not teach or suggest the production of a fusion protein comprising histone deacetylase and a DNA binding protein, and therefore does not disclose the or suggest the method as defined in claim 1, or the sequences as defined in claim 9. Thus, Applicants submit that a person of skill in the art, without the benefit of hindsight analysis, would not be motivated to combine the two references, nor would any combination teach or render obvious the present claims.

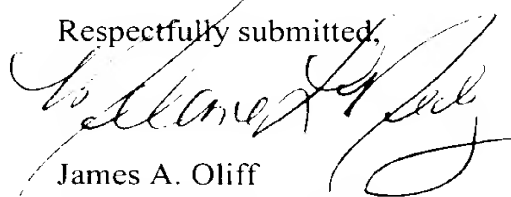
As claims 2-8 and 14-16 depend from claim 1, and claims 10-13, and claim 17-19 depend from claim 9, and include the limitations of claims 1 and 9 respectively, Applicants request withdrawal of Examiner's rejection of claims 1-9 and 11-20 under 35 U.S.C. 103(a).

VII. Conclusion

In view of the foregoing amendments and remarks, Applicants submit that this application is in condition for allowance. Favorable reconsideration and prompt allowance of the application are earnestly solicited.

Should the Examiner believe that anything further would be desirable in order to place this application in better condition for allowance, the Examiner is invited to contact Applicants' undersigned representative at the telephone number set forth below.

Respectfully submitted,



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Attachments:

Abstract
Appendix
Letter to the Official Draftsperson

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